

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 1, 2003, 08:45:46 ; Search time 25 Seconds
(without alignments)
744.915 Million cell updates/sec

Title: US-09-768-781-3

Perfect score: 2316

Sequence: 1 MDRVYIEPFPNDPVSSLE.....RTRVENSEPPFTEARQSVV 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	925	39.9	444	1	XX HUMAN
2	191.5	8.3	159	1	XXRY HUMAN
3	106.5	4.6	497	1	DTPT LACHE
4	105.5	4.6	1584	1	BAIL HUMAN
5	104.5	4.5	741	1	YBIO ECOLI
6	102.5	4.4	405	1	YMP0 YEAST
7	102.5	4.4	521	1	YT25 CAEEL
8	100.5	4.3	264	1	ATP6 PODAN
9	100.5	4.3	459	1	NU4M CERSI
10	99	4.3	233	1	ATPI OCHNE
11	99	4.3	458	1	ACHO HUMAN
12	98.5	4.3	456	1	G64A DROME
13	98.5	4.3	684	1	TC10 YEAST
14	98.5	4.3	1033	1	YD56 SCHPO
15	97.5	4.2	325	1	MCSR RAT
16	97.5	4.2	551	1	VPH1 YEAST
17	96.5	4.2	805	1	YB81 SCHPO
18	96	4.1	406	1	HOF6 HAEIN
19	95.5	4.1	252	1	ATP6 NEUR
20	95.5	4.1	255	1	ATP6 YARLI
21	95.5	4.1	325	1	MCSR MOUSE
22	95	4.1	430	1	REFB SALTY
23	95	4.1	692	1	NU5C MARPO
24	94.5	4.1	382	1	CKD6 RAT
25	94.5	4.1	438	1	MNT2 PSEAE
26	94.5	4.1	468	1	CBIA FUGRU
27	94.5	4.1	786	1	APEI SULTO
28	94	4.1	607	1	NU5M MOUSE
29	94	4.1	715	1	LCCL LACIA
30	93.5	4.0	2376	1	YIM9 YEAST
31	92.5	4.0	371	1	NY6R YEAST
32	92.5	4.0	552	1	NU5M RHISA
33	92	4.0	248	1	ATPI MARPO

34 92 4.0 455 1 ACHO CHICK
35 92 4.0 576 1 NUSM ANOQU
36 91.5 4.0 378 1 CKR7 MOUSE
37 91.5 4.0 429 1 SECY AQUAE
38 91.5 4.0 464 1 NU4M PARLI
39 91.5 4.0 628 1 YB1F SCHPO
40 91 3.9 298 1 FIG1 YEAST
41 91 3.9 394 1 G22A DROME
42 91 3.9 1597 1 RLRI YEAST
43 90.5 3.9 408 1 G58B DROME
44 90.5 3.9 567 1 DSB8 CAMJE
45 90 3.9 382 1 NU2M CHLRE

ALIGNMENTS

RESULT 1
XX_HUMAN STANDARD; PRT; 444 AA.
AC PS1811;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Membrane transport protein XK (Kx antigen).
GN XK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94273191; PubMed=8004674;
RA Ho M., Chelly J., Carter N., Danek A., Crocker P., Monaco A.P.;
RT "Isolation of the gene for McLeod syndrome that encodes a novel
RT membrane transport protein.";
RL Cell 77:869-880(1994).
RN [2]
RP REVISIONS TO 204-205.
RA Ho M.;
RL
CC -!- FUNCTION: MAY BE INVOLVED IN SODIUM-DEPENDENT TRANSPORT OF NEUTRAL
CC -!- AMINO ACIDS OR OLIGOPETIDES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN SKELETAL MUSCLE, HEART, BRAIN,
CC AND PANCREAS; LOW LEVELS IN PLACENTA, LIVER, AND KIDNEY.
CC -!- POLYMORPHISM: XK IS RESPONSIBLE FOR THE KX BLOOD GROUP SYSTEM.
CC -!- DISEASE: DEFECTS IN XK ARE THE CAUSE OF MCLEOD SYNDROME, AN X-
CC LINKED MULTISYSTEM DISORDER CHARACTERIZED BY ABNORMALITIES IN THE
CC NEUROMUSCULAR AND HEMATOPOIETIC SYSTEMS.
CC
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CC
CC EMBL; Z32684; CAA83632.2; --
CC Genew; HGNC:12811; XK.
CC
CC Transmembrane; Transport; Amino-acid transport; Blood group antigen.
CC
CC DOMAIN 1 2
CC TRANSMEM 3 23 POTENTIAL.
CC TRANSMEM 24 37 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 38 58 POTENTIAL.
CC TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 POTENTIAL.
CC TRANSMEM 90 140 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 141 161 POTENTIAL.
CC TRANSMEM 162 171 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 172 192 POTENTIAL.

FT DOMAIN 193 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229 POTENTIAL.
FT DOMAIN 230 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 298 POTENTIAL.
FT DOMAIN 299 317 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 318 338 POTENTIAL.
FT DOMAIN 339 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 370 POTENTIAL.
FT DOMAIN 371 444 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 444 AA; 50902 MW; 6F90B0B45659A1DA CRC64;
Query Match 39.9%; Score 925; DB 1; Length 444;
Best Local Similarity 44.5%; Pred. No. 2.4e-60;
Matches 179; Conservative 80; Mismatches 133; Indels 10; Gaps 4;
QY 33 PPSILSTFLYCGEASALYVRIYKNSERYMTYTFSPFMSSIMVQLTLIFVHRDL 92
DB 3 FPASVLASVPLFAETTAALSLSSTYRGDRMQALTLLFSLPCALVQLTLFVHRDL 62
QY 93 AKDKPLSLFHLILLGPVIRCLEAMIKYLTWKKEQEPEYVSLTRKK-MLIDGEEVLIE 151
DB 63 SRDRPLVLLHLLQLGLPFRFCFEVCIY---FQSGNNEEPYVSIITKQMPKQGLSEBIE 119
QY 152 WEVCHSIRTLAWHRNAYKMSQIQAPLGSVQLTYQLVLSISARVPLGRVVLVFLSVLS 211
DB 120 KEVGOAEGKLTHTRSASFASRASVIOAPLGSAPQLTYQLVLSVQMDDVTYVGRSLMTISLS 179
QY 212 VTYGATLCNMLAIOIKYDDYKIRLGPFLVLCITIMRTLEITSRLILVLSATLKLKAVP 271
DB 180 IVGALRCNLAIAIKYDEYEVKVKPLAYVLCIFLWRSFEIATRVVVLVFLTSVLTWVVV 239
QY 272 FLVNLFIILPEPWIKFWRSGAQMNNIEKNFSRVGTGLVWLISVTLVYAGINFSCWSALQ 331
DB 240 IILNFFSFPLYPWILFCWCSGSPPEKALSRVGTIVLCFLTLVYTGINMFCWSAVQ 299
QY 332 LRLADRLVDKGQWGHMGLHYSLVENVIMVLVFKFGVKVLLNCHSLIALQLIATY 391
DB 300 LKIDSPILSKSHNWYQLVYVYIMRFINAILLWLYLFKTDIYVVCAPLLVLQLLIGY 359
QY 392 LISIDFLLFQYLPLRLSLFTHNVD---YLHCVC--CHQ 427
DB 360 CTALFLMVFYQFHPCKKLSSSVSEGFQWLRCFCWACRQ 401

RESULT 2
XKRY HUMAN STANDARD; PRT; 159 AA.
AC O14609; (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Testis-specific XK related protein Y.
GN XKRY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98022381; PubMed=9381176;
RX Lahn B.T., Page D.C.;
RA "Functional coherence of the human Y chromosome.";
RL Science 278:675-680(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
CC -1- SIMILARITY: SOME, TO MEMBRANE TRANSPORT PROTEIN XK.
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CC EMBL: U77486; AAC45382.1; --
DR InterPro: IPR000109; PTR2.
DR Pfam: PF00854; PTR2; 1.
DR TIGRFAMs: TIGR00923; 2A1701; 1.
DR PROSITE: PS01022; PTR2; 1.
DR PROSITE: PS01023; PTR2; 2; 1.
KW Peptide transport; Transport; Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 26 46

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CC or send an email to license@isb-sib.ch).
CC EMBL: AF000997; AAC51844.1; --
DR Genew; HGNC:18571; XKRY.
DR MIM; 400015; --
KW Transmembrane.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 45 65 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
SQ SEQUENCE 159 AA; 18083 MW; B9E81DD842DEFOAB CRC64;
Query Match 8.3%; Score 191.5; DB 1; Length 159;
Best Local Similarity 31.2%; Pred. No. 1.9e-07;
Matches 45; Conservative 39; Mismatches 51; Indels 9; Gaps 4;
QY 206 VFSLSVTYGATLCNMLAIOIKYDDYKIRLGPFLVLCITIMRTLEITSRLILVLSATL 265
DB 11 IFPLISCV-GAHCNLAIRTGNDFAAIKLQVILYLMHSLVLIISPVVTLAFPPASL 69
QY 266 KLKAVPFLVNLFIILPEPWIKFWRSGAQMNNIEKNFSRVGTGLVWLISVTLVYAGI--- 322
DB 70 KQGSILHFLIITYFVLLITPMLFEFSKSGTHLPSTNK---IIPAWVVSMDAYLNHASICCH 125
QY 323 NFSCWSALQLRLADRLVDKQGNW 346
DB 126 QFSLSAVKQLQSLNEELI-RDTRW 148
RESULT 3
DTPT LACHE STANDARD; PRT; 497 AA.
AC O07380;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DI-/tripeptide transporter.
GN DTPT.
OS Lactobacillus helveticus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1587;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCDO 2712;
RX MEDLINE=97316430; PubMed=9172341;
RA Nakajima H., Hacting A., Kunji E.R.S., Poolman B., Konings W.N.;
RT "Cloning and functional expression in Escherichia coli of the gene
RT encoding the di- and tripeptide transport protein of Lactobacillus
RT helveticus";
RL Appl. Environ. Microbiol. 63:2213-2217(1997).
CC -1- FUNCTION: PROTON-DEPENDENT UPTAKE OF DI- OR TRI-PEPTIDES.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
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CC EMBL: U77486; AAC45382.1; --
DR InterPro: IPR000109; PTR2.
DR Pfam: PF00854; PTR2; 1.
DR TIGRFAMs: TIGR00923; 2A1701; 1.
DR PROSITE: PS01022; PTR2; 1.
DR PROSITE: PS01023; PTR2; 2; 1.
KW Peptide transport; Transport; Transmembrane.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 26 46

```
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 227 247 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
FT TRANSMEM 321 341 POTENTIAL.
FT TRANSMEM 372 392 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
SQ SEQUENCE 497 AA; 55469 MW; 69C064FFP9A0A26A5 CRC64;

Query Match 4.6%; Score 106.5; DB 1; Length 497;
Best Local Similarity 20.8%; Pred. No. 1;
Matches 85; Conservative 65; Mismatches 133; Indels 125; Gaps 18;

QY 91 DLAKDKPLSLFMHLLILGPVIR-----CLEAMI 118
Db 110 DPRDAGSIFVFGINLGSIIAPMLVPWAAQGVHIFGSQLNFHAGFSLAAGVGFGLV 169
QY 119 KYLPLWKKEOEPEPVSLTRKMLIDGEEV-LIEWEVGHSIRTLAMHRNAYKRMSQIOAF 177
Db 170 QYVLGGKYLSTE---SLTPNDPKDGLNLVKKVVIITAIIVA-----ILAA 215
QY 178 LGSVPQTYQLYVSL---ISAEVPLGRVYLMVFS--LVSVTYGATLCNM----- 221
Db 216 MAGVQLSDVNIVLTLLTALATLPIYVPMFRSSKVTKIELGIHLLPVLKNRLFPPKKG 275
QY 222 -----LAIQIKYDDYKIRLGPVLCVITWRTLEITSLRLILVLF-SATLKLKAVP 271
Db 276 YKRLKQIQLLEAIKROSFILIALIIMASILIPNKVIAKHLKLVLVYVWIGLNLIP 335
QY 272 F--LVNLFILPEPWIK--FWRSGAQPNNIEKN-----FSR-----VGTLLVL 312
Db 336 FSTFVLFS--LFDYIKHMPKKEGEQAKTKERSIHGIEIPLFLQLIINIFTLIL 392
QY 313 ISVTIL-YAGINFSC-----WSALQLRLADRLVDKQNGHMGHLYSVRLVENIMV 364
Db 393 EGETLPDENGVEVNIAPHPVQGYTELNLINKSDILWADW-----IQSV--- 438
QY 365 LVPKFFGVKVLNLYCHSLALQLLIAYLISIDFMLFPQYLHPLRSLF 412
Db 439 -----AKYLLNIMYADVIVIIIFVLKMAALWMAWSYI-PLSTVF 478
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RESULT 4

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BAI_HUMAN STANDARD; PRT; 1584 AA.
AC O14514;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brain-specific angiogenesis inhibitor 1 precursor.
GN BAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98054121; PubMed=9393972;
RA Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K.,
RA Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Tokino T.;
RT "A novel brain-specific p53-target gene, BAI1, containing
RT thrombospondin type 1 repeats inhibits experimental angiogenesis.";
RL Oncogene 15:2145-2150(1997).
RN [2]
RP INTERACTION WITH BAP1.
RX MEDLINE=98321173; PubMed=9647739;
RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
RA Tokino T.;
RT "Cloning and characterization of BAI-associated protein 1: a PDZ
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RT domain-containing protein that interacts with BAI1.";
RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
CC -!- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN
CC BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P53
CC SIGNAL IN SUPPRESSION OF GLOBLASTOMA. MAY FUNCTION IN CELL
CC ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.
CC -!- SUBUNIT: INTERACTS WITH BAP1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE
CC CONCENTRATED AT CELL-CELL ADHESION SITES.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED OR NO
CC EXPRESSION IS OBSERVED IN SOME GLOBLASTOMA CELL LINES AND CANCER
CC TISSUES.
CC -!- INDUCTION: BY P53.
CC -!- DOMAIN: THE TSPI REPEATS INHIBIT IN VIVO ANGIOGENESIS IN RAT
CC CORNEA INDUCED BY BFGF.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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CC -----
DR EMBL; AB005297; BAA23647.1; -.
DR Genbank; HGNC:943; BAI1.
DR MIM; 602682; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR002023; PKD_cys_rich.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF00090; tsp_1; 5.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; Hormr; 1.
DR SMART; SM00209; TSPI; 5.
DR PROSITE; PS50221; GPS; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS50092; TSPI; 5.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
DR Repeat; Cell adhesion.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1584 BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1.
FT DOMAIN 31 948 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 949 969 1 (POTENTIAL).
FT DOMAIN 970 980 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 981 1001 2 (POTENTIAL).
FT DOMAIN 1002 1008 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1009 1029 3 (POTENTIAL).
FT DOMAIN 1030 1052 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1053 1073 4 (POTENTIAL).
FT DOMAIN 1074 1093 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1094 1114 5 (POTENTIAL).
FT DOMAIN 1115 1136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1137 1157 6 (POTENTIAL).
FT DOMAIN 1158 1166 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1167 1187 7 (POTENTIAL).
FT DOMAIN 1188 1584 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 261 316 TSP TYPE-1 1.
FT DOMAIN 354 408 TSP TYPE-1 2.
FT TRANSMEM 409 463 TSP TYPE-1 3.
FT DOMAIN 467 521 TSP TYPE-1 4.
FT TRANSMEM 522 576 TSP TYPE-1 5.
FT DOMAIN 881 938 GPS.
FT DOMAIN 1411 1422 POLY-PRO.
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DNA Res. 3:137-155(1996).
RL  -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC  -1- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.
CC  -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC      frameshift in position 77.
CC -----
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CC -----
DR  ENBL; AAC73895.1; ALT_INIT.
DR  ENBL; D90717; BAA35474.1;
DR  ENBL; D90718; BAA35479.1; ALT_FRAME.
DR  ENBL; D90719; BAA35480.1; ALT_FRAME.
DR  EcoGene; EGI3320; ybio.
DR  InterPro; IPR001880; MSion channel.
DR  Pfam; PF00924; MS channel_1.
DR  PROSITE; PS01246; UPF0003; FALSE_NEG.
KW  Hypothetical protein; Transmembrane; Complete proteome.
FT  TRANSMEM 9 29 POTENTIAL.
FT  TRANSMEM 143 163 POTENTIAL.
FT  TRANSMEM 185 205 POTENTIAL.
FT  TRANSMEM 225 245 POTENTIAL.
FT  TRANSMEM 268 288 POTENTIAL.
FT  TRANSMEM 294 314 POTENTIAL.
FT  TRANSMEM 343 363 POTENTIAL.
FT  TRANSMEM 374 394 POTENTIAL.
FT  TRANSMEM 432 452 POTENTIAL.
FT  TRANSMEM 466 486 POTENTIAL.
FT  TRANSMEM 509 529 POTENTIAL.
FT  TRANSMEM 533 553 POTENTIAL.
FT  TRANSMEM 562 582 POTENTIAL.
FT  TRANSMEM 608 628 POTENTIAL.
FT  TRANSMEM 662 682 POTENTIAL.
FT  DOMAIN 25 30 POLY-THR.
FT  DOMAIN 195 202 POLY-LEU.
FT  SEQUENCE 741 AA; 81903 MW; 69B0A27678976DB5 CRC64;
Query Match 4.5%; Score 104.5; DB 1; Length 741;
Best Local Similarity 19.5%; Pred. No.2,3;
Matches 96; Conservative 91; Mismatches 173; Indels 133; Gaps 25;
Qy 1 MDRVETPEEPNDVPVSSLEEDVIRGANPRFTFFSLFSTFL-----YCGEASAL 52
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
66 IDQLRTVAATPPAPPV-----PRIVPTLVEEQTVLQKVTEVSRHYGEALSAR 113
Qy 53 YMVRIYRK-----NSETYRTVT-----PSFFMFSSIMVQLTLFVHRDLA- 93
Db 114 F-GOLYRNITGSPHKPNPTFSNALTHFSMLAVLVGFIW----LRLCALPYRQMGQ 168
Qy 94 ----KQKPLSLFMHL--ILLGPVIRCLEAMIKYLTLMKKKEEBEPYVSLTRKKMLDGE 147
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
169 WARQKNRERNWLQLPAMIIGAFI-IDLLALLALTLPVQG----- 206
Qy 148 VLIEWEVGHSIRTLAMERNAYKRMSQIQAFGLGSPQLTY-----QLVSVLSARVP--LG 200
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
207 -LVSDNLNAGSRITAFQOQSLFNALFIEFKAFLRILFCPNVAELPFTIQDESARYWS 265
Qy 201 RVLWMFSLSVVYGTATCNMLAIOIKYDDYDKIRIGPLE---VLCITIW-----RTL 249
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
266 RRLSWLSSLIG--YGL-----IVAPPIISQNVOIGALANVIMLCVTWVALYLFNKK 319
Qy 250 EITSRL-----ILVFSATLK-----LKAVPFVLVNLFLIILPEFPWIKFWRSGAQM 296
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
320 EITQHLNFAEHSLAPSLFIRAFALVWHHLASAYFIVL-FFFSLPDP-----G 367
Qy 297 NNTKPNFRVGTLLVILISVTILVAGINFSCWALSQLRKADR-----DLVDKQNWGHMG 350
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
368 NSLKFMFGATVRSIIAIGIAAFVSGM-FSWLAKTIFLSPHTORNYPELOKRLNGWLSAA 426

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FT IRANSHEM 682 POLY-THR.
FT DOMAIN 25 POLY-LEU.
FT DOMAIN 195 POLY-LEU.
SQ SEQUENCE 741 AA; 81903 MW; 69B0A27678976DB5 CRC64;

Query Match 4.5%; Score 104.5; DB 1; Length 741;
Best Local Similarity 19.5%; Pred. No. 2.3;
Matches 96; Conservative 91; Mismatches 173; Indels 133; Gaps 25;

Qy 1 MDRVYEPEEPNVDYVSSLEEDVIRGANPFTPEFSILFSTFL-----YCEAASAL 52
Db 66 IDQURTVAAETPAEPV-----PKIVPPTLVEEQTVLQKVTESRHYGEALSAR 113
Qy 53 YMVRIRYRK-----NSETRYMTYT-----FSFFMFSSIMVQLTLIFVHRLA- 93
Db 114 F-GOLYRNITGSPHKPNPQTFSNALTFHSMALVLFVGFYW---LIRLCALPLYRKMGG 168
Qy 94 ----KOKPLSLFHWL---ILLGPVIRCLAEAMKLYTLWKKEEQEPEYVSLTRKQMLIDGEE 147
Db 169 WAROKNRSRNMWLQPLAMITCAFT--IDLLLLALTLPVGG-----206
Qy 148 VLIEWEVGHSIRTLAMHERNAYKMSQIQAFUGSVPOLTY-----QLVVSLSIAEVP--LG 200
Db 207 -VLVDNLNAGSRITAFQOGLFNAFLIEPFKAVLRIFCFNVAELRPFPTIODESARYWS 265
Qy 201 RVLMWPSLVSVMYGTATCNMLAIQIKYDDYKIRGLPLE---VLCTITW-----RTL 249
Db 266 RLISWLSLIG--YGL-----IVAVPIISQNVQIGALANVIMLCMTVWALYLI FRNKK 319
Qy 250 EITSRLD---ILVLFSA TLK-----LKAVPFVLVLNPLILFEPWIKFWRSGAQM 296
Db 320 EITQHLNFAEHSIAPSLFIRAFALVWHWLASAYFVLV-FFSFLDP-----G 367
Qy 297 NNTKXPSRVGTLVWLISVTILVAGNFCWSALQLKLADR-----DLVDKQNWGHMG 350
Db 368 NLSKFMFMGATVRSIIAIGIAAFVSGM-FSWLAKTITFLSPHTORNYPELOKRLNGLWSAA 426

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Db 162 -----IALTHIQNLGTSLNLL---IQYSTQTLPSWSNAFLWACMM 201

QY 176 AFIGSVPOLTYQLVSLISAEVPL-GRVLMVFSLVSUTYGATLCNMLAIQIKYDDYKIR 234

```

Db 202 AFVVKMPGLYGLHLWLPKARVEAPTAGSNVLAAILLKGQYGLRMTMI----- 249
Qy 235 LGPL-----EVLCTITWRTLEITSRLILVLPATLKLKAVPFLVNLFLILFE-PWIK 287
Db 250 LNPFTSYMAFPFLMSLWGMIMTSSICLRQDLSLAIYSSVSHMALVIVAVLIQTWP-S 308
Qy 288 FWRSGAQM-----PNNIEKNFSR-----VGTLVVLSVTLYIYAGINFSC 326
Db 309 YMGATALMIAHGLTSSVLFCLANSYERTHSRTMLARGLOTLLPLAMWWLLASLT--- 365
Qy 327 WSALQLRLADRLVDKQNGHGMGLHYSRVLVENIWL-VKPFQGVKVLNLYCHSLIAL 385
Db 366 -----NLALPPTINLVGELFVMSFSNSNITII-----LMGT 398
Qy 386 QLIHAIYISIDFMLFFOYLHPLRSLETHNVVDVLCVCHQHQRTRVENSEPFFETE 443
Db 399 NIIITALYSL-YMLITTO-----RGKYTHH-----INNKPSTFRE 433

RESULT 10
ATPI OCHNE
ID ATPI OCHNE STANDARD; PRT; 233 AA.
AC Q40607;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase A chain precursor (EC 3.6.3.14) (Subunit IV).
GN ATPI.
OS Ochrosphaera neapolitana.
OC Chloroplast.
OC Eukaryota; Haptophyceae; Isochrysidales; Ochrosphaera.
OX NCBI_TaxID=35137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCMP 593;
RA Huss V.A.R., Tietze A.C., Julius C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC H(+) (out).
CC -1- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
CC thylakoid membrane.
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC
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CC
CC EMBL; X99078; CAA67535.1; -.
CC InterPro; IPR000568; ATPsynT_Asub.
CC Pfam; PF00119; ATP-synt_A; 1.
CC TIGRFAMs; TIGR01131; ATP_synt_6_or_A; 1.
CC PROSITE; PS00449; ATPASE_A; 1.
CC Hydrogen ion transport; CF(0); Chloroplast; Transmembrane; Signal.
CC SIGNAL 1 ? BY SIMILARITY.
CC CHAIN ? 233 ATP SYNTHASE A CHAIN.
CC FT TRANSMEM 27 47 POTENTIAL.
CC FT TRANSMEM 84 104 POTENTIAL.
CC FT TRANSMEM 192 212 POTENTIAL.
CC SEQUENCE 233 AA; 25721 MW; 6EEA74DE0887D6F1 CRC64;
Query Match 4.3%; Score 99; DB 1; Length 233;
Best Local Similarity 23.7%; Pred. No. 1.6;

```

```

Matches 64; Conservative 22; Mismatches 68; Indels 116; Gaps 13;
Qy 205 MVFSLVSVTVYGTATCNMLAIOIKYDDYKIRLGPLE-----VLCITWRTLEITSRLILVL 260
Db 1 MFFSLAAVEVTHL-----YWEIGGLEVHGQVLLIT-WLVLAAILTLAIL-- 44
Qy 261 FSATLKLKAVPFLVNLFLILFE-----PWIKF-----WRSG 292
Db 45 --GTLKLEQVFKQNFLESFEYVSGIAKQDIGYHYRPMVPFVGTFLFIFVANW-LG 101
Qy 293 AQMP-----NNIEKNFSRVGTILVLSVTLYIYAGINFSCWSALQLRLADR 337
Db 102 ALIPKWLHLPEGLAAPTNDINTTVA-----LSLTSISYFYAGFK----- 143
Qy 338 DLVDKQNGHGMGLHYSRVLVE-----NVI-----MVLVKPFQ-----VKVL 375
Db 144 -----EKGIGFFARYISPTPIFLPINILEDTKPLSLFRFLGNLAIDEIVSVL 193
Qy 376 LNYCHSLIALQLIIAYLISIDFMLFFOYL 405
Db 194 CLLVPLLIPLPVMVIGIPASSVQALVFSTL 223

RESULT 11
ACHO HUMAN
ID ACHO HUMAN STANDARD; PRT; 458 AA.
AC Q05901; Q15827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, beta-3 chain precursor.
GN CHRN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Substantia nigra;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelbi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pons;
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5 and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Keddache M., Durner M., Greenberg D.A.;
RT "Genomic structure and mutation analysis of the CHRN3 gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 36-458 FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=9339761; PubMed=7690916;
RA Willoughby J.J., Ninkina N.N., Beech M.M., Latchman D.S., Wood J.N.;
RT "Molecular cloning of a human neuronal nicotinic acetylcholine
RT receptor beta 3-like subunit.";
RL Neurosci. Lett. 155:136-139(1993).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

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CC CC MEMBRANE.
CC CC -|- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC CC TYPE OF SUBUNITS: ALPHA AND BETA.
CC CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC CC
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CC CC
CC CC EMBL; U62438; AAB40116.1; -
CC CC EMBL; Y08417; CRA69694.1; -
CC CC EMBL; AF140765; AAD33063.1; -
CC CC EMBL; AF140760; AAD33063.1; JOINED.
CC CC EMBL; AF140761; AAD33063.1; JOINED.
CC CC EMBL; AF140762; AAD33063.1; JOINED.
CC CC EMBL; AF140763; AAD33063.1; JOINED.
CC CC EMBL; AF140764; AAD33063.1; JOINED.
CC CC EMBL; X67513; CAA47851.1; -
CC CC PIR; S25587; S25587.
CC CC Genew; HGNC:1963; CHRN3.
CC CC
CC CC MIM; 118508; -
CC CC InterPro; IPR000188; GABAA receptor.
CC CC InterPro; IPR001175; Neur_channel.
CC CC Pfam; PF02931; Neur_chan_LBD; 1.
CC CC Pfam; PF02932; Neur_chan_memb; 1.
CC CC PRINTS; PR00252; NRIONCHANNEL.
CC CC TIGRFAMs; TIGR00860; LIC; 1.
CC CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC CC Transmembrane; Multigene family.
CC CC SIGNAL 1 24
CC CC CHAIN 25 458
CC CC
CC CC DOMAIN 25 232
CC CC TRANSMEM 233 257
CC CC TRANSMEM 265 282
CC CC TRANSMEM 299 320
CC CC DOMAIN 321 428
CC CC TRANSMEM 429 447
CC CC DISULFD 153 167
CC CC CARBOHYD 51 51
CC CC CARBOHYD 138 138
CC CC CARBOHYD 166 166
CC CC CONFLICT 36 38
CC CC LPO -> EWK (IN REF. 3).
CC CC SEQUENCE 458 AA; 52728 MW; D6E919E53CBD21F8 CRC64;
CC CC
CC CC Query Match 4.3%; Score 99; DB 1; Length 458;
CC CC Best Local Similarity 25.7%; Pred. No. 3.3;
CC CC Matches 45; Conservative 35; Mismatches 63; Indels 32; Gaps 8;
CC CC
CC CC Qy 73 PFMESSIMVQLTLLI---FV---HRLAKDKPLSLPMHLILG--PVIRCLEAMIKYLT 123
CC CC Db 299 YLLFTMIPTLLSIITVTVINVHRRSSSTYHPAPWKKLFQKLPKLCMKDHDVDRYS 358
CC CC
CC CC Qy 124 WKKEQEPEPYV-----SLTRKMKLIDGEEVLIEW--EVGHSIRTLAMHRYNAYKMSQIOA 176
CC CC Db 359 PEKEE-SQPVKGVKLEKKQKQSDGKVLAFLEKAADSIRYSRHVKEHFTISQVQV 417
CC CC
CC CC Qy 177 FLGSPVQTLTYQLYVLSIAEVPGLGRVVLVSVTVYATLGNMLAIGIKYDDY 231
CC CC Db 418 DWKFVAQV-----LDRIFLFLFLIVSVT-GSVLIPTALKWMLHSY 457
CC CC
CC CC RESULT 12
CC CC G64A DROME
CC CC ID G64A DROME STANDARD; PRT; 456 AA.
CC CC AC P83293; Q9VZJ7;
CC CC DT 15-JUN-2002 (Rel. 41, Created)

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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative gustatory receptor 64a.
GN GR64A OR CG14986.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP IDENTIFICATION.
RX MEDLINE=21407712; PubMed=11516643;
RA Dunipace L., Meister S., McNealy C., Amrein H.;
RT "Spatially restricted expression of candidate taste receptors in the
RT Drosophila gustatory system."
RL Curr. Biol. 11:822-835(2001).
RN [3]
RP CONCEPTUAL TRANSLATION.
RA Robertson H.;
RL Unpublished observations (NOV-2001).
CC -|- FUNCTION: Probable role in the gustatory response.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN COUPLED
CC RECEPTORS. SUBFAMILY II.
CC -|- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC
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EMBL; A5003480; AAF47824.1; ALT_SEQ.
FlyBase; FBgn0045479; Gr64a.
Hypothetical protein; Receptor; G-protein coupled receptor;
Transmembrane; Glycoprotein; Multigene family.
DOMAIN 1 61
TRANSMEM 62 82
DOMAIN 83 95
TRANSMEM 96 116
DOMAIN 117 128
TRANSMEM 129 149
DOMAIN 150 185
TRANSMEM 186 206
DOMAIN 207 238
TRANSMEM 239 259
DOMAIN 260 321
TRANSMEM 322 342
DOMAIN 343 351
TRANSMEM 352 372
DOMAIN 373 456
TRANSMEM 457 52
CARBOHYD 52 52
TRANSMEM 217 217
SEQUENCE 456 AA; 52822 MW; 5466974CT3495D6C CRC64;

Query Match 4.3%; Score 98.5; DB 1; Length 456;
Best Local Similarity 20.7%; Pred. No. 3.6;
Matches 75; Conservative 60; Mismatches 117; Indels 111; Gaps 21;

QY 8 PEPNVDPV--SSLEEDVIRGAN-PRT-----PPSILSTFLYCGEASALVMV 55
DB 27 PETPPKPFVEDSNLEFNVLASEKLPNTNLDLFRVFP-----FMFLAQCVAIMPLV 79
QY 56 RIYKNSSETMYT-TFSFFMFSSIMVQLTLIFVHRDLAKDKPLSLFMHLLILGQVIR-- 112
DB 80 GIRESPRRVRFAKSPIMFVTLFIATISLF-----LSMFTHLLKIGITAKNF 129
QY 113 -----CLEMKIYTL-----WKKE-----QEPYVSLTRKMLIDGEE 147
DB 130 VGLVFGCVLSAYVVFVIRLAKWPVAVIRTRTEIPKPYEIPKRNLSRVQL---AA 186
QY 148 VLIEWEYGHISIRTLAMH-----NAYKMSQIQAFGLGVP-----OLTYQYVLSISAEV 197
DB 187 LAI---IGLSGEHALYQVSAISITRIQCANITTVPSFNNVQNTYDVFQLL----- 239
QY 198 PLGRVLMVFLSVSVTYGATLCNNL-----AIOIKYDDYKIRGLPL--EVLIC 242
DB 240 PYSPIIAVLLIN--GA--CTFVWYMDLFIMWISKLSYRFEQITTRKLEHEEVC 294
QY 243 ITTW-----RTLE-ITSRLILVLSATLKLKAVPFLVNLFIILFEP--WIKF 288
DB 295 ESFVIQIREHYVVKMCELLEFVDSAMSSILLSCVNNLYFVCYQLNFKLRWPNINYIF 354
QY 289 WRS 291
DB 355 WYS 357

RESULT 13

TC10_YEAST STANDARD; PRT; 684 AA.
ID TC10_YEAST
AC P50273;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE TC10 protein.
GN TC10 OR YDR350C OR D9476.9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RN SEQUENCE FROM N.A.
RP STRAIN=MH125;
RA Zhang Y., Robinson K.M., Lemire B.D.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]

SEQUENCE FROM N.A.
RP Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Fucillo A., Fullon L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevasakis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]

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EMBL; U32306; AAA74031.1; -;
DR EMBL; U28372; AAB64786.1; -;
DR SGD; S0002758; TCM10.
DR CONFLICT 592 684
FT GARSWYNKILFGGEIRHMAIOIKDOGWPPKPNFDETL
FT TELVENNIKPEPTDSTLTDEDMFEEDGKPRNDODVNKCT
FT NIIRTEKLSN -> EHAPGTRYSSGALKSGIWL (IN
FT REF. 2).

QY SEQUENCE 684 AA; 79755 MW; A88992848F8F49A4 CRC64;
Query Match 4.3%; Score 98.5; DB 1; Length 684;
Best Local Similarity 18.7%; Pred. No. 5.7;
Matches 90; Conservative 60; Mismatches 163; Indels 169; Gaps 19;

QY 31 FTFFPFSILSTFLYCGEASALVMVRIYKNSSETMYTTFSTFFM----- 75
DB 173 FLKSDVLLFTSNCTFTNRLI-----KGTMERQATQIFLHDETNIKFIMEKVUK 226
QY 76 -----FSSIMVQLTL-----IFVHRDLAKDKPL-----SLF 101
DB 227 LHTFDSLIALVNLGVAKNPFKIFVFIQALLQLEQHCYSGKDGAKQKNLYVKFNNTLL 286
QY 102 MHLILLGPVIRCLAMIKYLTWKKEQEPYVSLTRKMLIDGSEVLEWEGHSIRTL 161
DB 287 YLLKSGNV---ELFIKTF-----QELKFIYSSGLLNHDGNEHILNPFHLYNL 336
QY 162 AMHFNAYKMSQIQAFGLGVPOLTYQYVLSISAEVPLGRVVMVFLSVSVTYGATLCNM 221
DB 337 RI-SNROEELFNVISCLQSSPIMKYKLKPEFLMG-----LIASFOAFRDPKLVCKY 387
QY 222 LAIQIKYDDYKIRGLPLEVLCITTWRTL-EITSRLILVLSATLKLKAVPELVNLFII 280
DB 388 L-----LSSYSKASANILNALGIWGLYHKSSTLTAPTARELNK----- 430
QY 281 LFEPWIKFWRSGAQMNNIEKNFGRVGLVLIISVTILYAGINFSCWSALQRLADRLV 340
DB 431 -----NNILPNTMRIGSPVTPILTLYRSLLSS--SSVSL----- 464
QY 341 DKGQWGHMGLHYSVRLVENVMVLFKFFG-----VKVLLNYCHSL 392
DB 465 ESGQ-----FKNCLDLYYKYSFLSEAHKYRYWRNDTGILNPLNYIR-F 510
QY 383 IALQLIITAYLISIDFMLLFFOYLHPL-----RSLETHNVVDYLHVCCHQHPTRVEN 435
DB 511 QAREPRLAYNVLLDF-----YSQFFAKKVLTITLCPFSIVAY-----KNHLTQASL 558
QY 436 SE 437
DB 559 SE 560

```

RESULT 14
YD56 SCHPO STANDARD; PRT; 1033 AA.
AC Q10309;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Potential phospholipid-transporting ATPase C6C3.06C (EC 3.6.3.1).
GN SPAC6C3.06C
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Uesery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002)
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(CC (E1-E2 ATPASES). SUBFAMILY IV.
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CC EMBL; Z69731; CAA93618.1; -
CC InterPro; IPR001757; ATPase_E1-E2.
CC InterPro; IPR001454; Hlgase/hydrolase.
CC Pfam; PF00702; Hydrolase; 1.
CC PROSITE; PS00154; ATPase_E1_E2; 1.
KW Hypothetical protein; Hydrolase; Transmembrane; Phosphorylation;
KW Magnesium; ATP-binding.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 344 364 POTENTIAL.
FT TRANSMEM 768 788 POTENTIAL.
FT TRANSMEM 843 863 POTENTIAL.
FT TRANSMEM 913 933 POTENTIAL.
FT TRANSMEM 939 959 POTENTIAL.
-----
FT TRANSMEM 965 985 POTENTIAL.
FT TRANSMEM 992 1012 POTENTIAL.
FT MOD RES 408 408 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 770 770 MAGNESIUM (BY SIMILARITY).
FT METAL 774 774 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 1033 AA; 116587 MW; D57C467427D0C6D6 CRC64;
Query Match 4.3%; Score 98.5; DB 1; Length 1033;
Best Local Similarity 19.8%; Pred. No. 9;
Matches 62; Conservative 55; Mismatches 91; Indels 105; Gaps 15;
QY 46 GEARAS--ALYMWVRIYRKNS-----TYRMTYTFSPFMFSIMVQLTLIFVHRDLAKD 95
DB 792 GQASLAADYSVKESHSVRLLLWHGRISYKQTSKLAFMVHRGLLISVCQVYSVISAF 851
QY 96 KPLSLFPMHLIILGPVIRCLEAMIKYLTWKKEEQEPEYVSLTRKMLDGEVLEWEVG 155
DB 852 EFIALFOGLLLVG-----YSTM-----YTMFVFSIVYDRDV----- 883
QY 156 HSRTLAMHRNAYKEMSOIOAFLGSPQLTYOLYVSLISAEPVPLGRVV-LMVFSLV---- 210
DB 884 -SEKLVFLFPELYKEMREQKCF-----SYKNFISCVLSIVYQGLIIQLFTFYLGFEF 935
QY 211 ----SVTYGATLCN---MLAIQIKYDDYKIRGLPLEVLCITIRWLTETSRLLIILVLS 262
DB 936 EGKMLAVCFSCLIFFNELIMVALQ-----INTWEQTIVMSELLTMMY- 977
QY 263 ATLKMAVFFVLNPLFIILFPWIKF-WRSGAQMNNIEKNFSRVGTLLVLSIVTILYAG 321
DB 978 ----ILSVPEFLT-NYFELKFLGLKFWY-----VSALIFLISLLPVM-- 1014
QY 322 INFSCWSALQRL 334
DB 1015 ----CGKALKRKL 1023
RESULT 15
MC5R RAT STANDARD; PRT; 325 AA.
AC P35345;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Melanocortin-5 receptor (MC5-R).
GN MC5R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Striatum;
RX MEDLINE=94234987; PubMed=8179577;
RA Griffon N., Mignon V., Facchinetti P., Diaz J., Schwartz J.C.,
RA Sokoloff P.;
RT "Molecular cloning and characterization of the rat fifth melanocortin
RT receptor."
RL Biochem. Biophys. Res. Commun. 200:1007-1014(1994).
CC -1- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
CC IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: VERY LOW EXPRESSION LEVELS IS DETECTED IN
CC BRAIN, WHILE HIGH LEVELS ARE FOUND IN ADRENALS, STOMACH, LUNG AND
CC SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; L27081; AAA41577.1; --
DR PIR; JC2193; JC2193.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 38 61 1 (POTENTIAL).
FT DOMAIN 62 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 97 2 (POTENTIAL).
FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 138 3 (POTENTIAL).
FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 156 179 4 (POTENTIAL).
FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 211 5 (POTENTIAL).
FT DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 265 6 (POTENTIAL).
FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 297 7 (POTENTIAL).
FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 311 311 PALMITATE (POTENTIAL).
FT LIPID 312 312 PALMITATE (POTENTIAL).
SQ SEQUENCE 325 AA; 37050 MW; 4E19FF1ABE8A6BDC CRC64;
Query Match 4.2%; Score 97.5; DB 1; Length 325;
Best Local Similarity 19.2%; Pred. No. 2.9;
Matches 64; Conservative 67; Mismatches 114; Indels 89; Gaps 17;
QY 131 EPYVSLTRKQMLDGEVLEWVGHSHIRTLAMRNAYKRNKSOIQAPLGSVPQL----- 184
Db 41 EVFLTLGLVSL-----ENILV---IGAIVKKNKLH-----SPMYFFVGS LAVADMLVSM 87
QY 185 -----TYQLYV---SLISAEVPLGRVVLVFLSVVGYGATLGNMLAIOI-KYDD--YK 232
Db 88 SNAWETITVILNNKHVVIADTFVRHIDNVFDSMICISVVASMSLLAIAVDRIITIFYA 147
QY 233 IRLGPL-----EVLCTITWRTLEITSRLLLVLFSA---TLKLKAVPPLVFLNFIILFE 283
Db 148 LRVHIMTARRSGVLIACIW-TPCISGIVFIYYESKYVIVCLISMFTMLFFMVSLYI 206
QY 284 PWIKFWRSG-----AOMP--NNIEKNFRVGLVVLVLSVTILYAGINFSCWSALQRLADR 337
Db 207 HMFLLARNHVKRIAASPRYNSVRQASMKGA-----ITLTM-LGIFIVCWSPPFLHLI-- 259
QY 338 DLVDKGNQWGHMGLHYSLRVLVENIVLVKPKFVGKVLNLYCHSLIALQLLIIVLISIDF 397
Db 260 -----LMISCPQNYCACFMSYFNWYLILINCNSVID----- 291
QY 398 MLLFFQYLHPLRSLFTHNVVDYLHCVCCHQHPRT 431
Db 292 -----PLIYALRSQEMERT--FKEIICCHGPRRT 318
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